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## WHAT IS CLAIMED IS:

- 1. A method of determining a base sequence for nucleic acid, electrophoresing a fragment sample of nucleic acid and determining the base sequence of the nucleic acid on the basis of detected data, comprising steps of:
- (A) performing waveform shaping by Fourier transformation on data of a certain number N of points from the head of the detected data with a parameter of a previously set peak interval;
- (B) determining the base sequence as to data of P points (P < N) from the head of the data of N points;
- (C) obtaining a peak interval from the result of the sequence determination;
- (D) performing waveform shaping by Fourier transformation on data of N points from a position returning by L points (L < M) from final data precedently subjected to the sequence determination with a parameter of a precedently obtained peak interval; and
- (E) determining the base sequence as to data of M points (M < N) of a central portion to be connected with data precedently subjected to the sequence determination among data of N points subjected to second or later waveform shaping, wherein

the steps  $(E) \rightarrow (C) \rightarrow (D)$  are repeated until data disappear or no analysis is required despite presence of data.

The method of determining a base sequence for nucleic acid 2. according to claim 1, wherein

FFT treatment is applied as the waveform shaping by Fourier transformation.

The method of determining a base sequence for nucleic acid

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according to claim 2, assuming that N is equal to  $2^n$ , M is equal to  $2^{(n-1)}$  and L is equal to  $2^{(n-2)}$ .